

SEQUENCE LISTING

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Steele, Doug
Jones, Robert M.

<120> Tau-Conotoxin Peptides

<130> Tau-Conopeptides

<140>
<141>

<150> US 60/118,642
<151> 1999-02-04

<160> 49

<170> PatentIn Ver. 2.0

<210> 1
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Generic
Sequence for Tau Conopeptides

<220>
<221> PEPTIDE
<222> (1)..(2)
<223> Xaa at residue 1 is Asp, Glu or gamma-carboxy-Glu
(Gla); Xaa at residue 2 is des-Xaa, Gln, Asn, Glu,
Trp (D or L), neo-Trp, halo-Trp, any unnatural
aromatic amino acid.

<220>
<221> PEPTIDE
<222> (3)..(4)
<223> Xaa at residue 3 is des-Xaa, Gly, Ala, Asn or Gln;
Xaa at residue 4 is des-Xaa4, Val, Leu (D or L),
Ile, Ala, Gly, Glu, Gla, Asp, Ser, Thr, Phe, Trp
(D or L), neo-Trp, halo-Trp (D or L) or any

<220>
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<222> (4)..(7)
<223> unnatural aromatic amino acid; Xaa at residue 7 is
Pro, hydroxy-Pro, Gln, Asn, Glu, Gla, Ala, Gly,
Lys, Arg, Ile, Val, homoarginine, ornithine,
N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys or

<220>
<221> PEPTIDE
<222> (7)..(8)
<223> any unnatural basic amino acid; Xaa at residue 8
is Val, Phe, Thr, Ser, Glu, Gla, Asp, Asn, Gln,
Ala, Gly, Ile, Leu (D or L), Met, Pro,

hydroxy-Pro, Arg, homoarginine, ornithine, Lys,
N-methyl-Lys,

<220>

<221> PEPTIDE

<222> (8)..(9)

<223> N,N,-dimethyl-Lys, N,N,N-trimethyl-Lys, any
unnatural basic amino acid or any unnatural
aromatic amino acid; Xaa at residue 9 is Val, Ile,
Asn, Leu (D or L), Gln, Gly, Ala, Phe, Glu, Gla,
Arg,

<220>

<221> PEPTIDE

<222> (9)..(10)

<223> ornithine, arginine, Lys, N-methy-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any
unnatural basic amino acid or any unnatural
aromatic amino acid; Xaa at residue 10 is Ile, Leu
(D or L), Met, Thr,

<220>

<221> PEPTIDE

<222> (10)

<223> Ser, Pro, hydroxy-Pro, Gln, Asp, Glu, Gla, Asn,
Arg, homoarginine, ornithine, Lys, N-methy-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, Tyr,
nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,

<220>

<221> PEPTIDE

<222> (10)..(11)

<223> O-phospho-Tyr, nitro-Tyr, any unnatural basic
amino acid, any unnatural aromatic amino acid or
any unnatural hydroxy containing amino acid; Xaa
at residue 11 is des-Xaa, Ala, Gly, Asp, Glu, Gla,

<220>

<221> PEPTIDE

<222> (11)

<223> Trp (D or L), neo-Trp, halo-Trp (D or L), Lys,
N-methy-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys, Arg, homoarginine, ornithine,
Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr,
O-sulpho-Tyr, O-phospho-Tyr,

<220>

<221> PEPTIDE

<222> (11)..(14)

<223> nitro-Tyr or any unnatural basic amino acid; Xaa
at residue 14 is des-Xaa, Ile, Leu (D or L), Val,
Glu, Gla, Asp, Thr, Ser, Pro, hydroxy-Pro, Trp (D
or L), neo-Trp, halo-Trp (D or L), Phe, any

<220>

<221> PEPTIDE

<222> (14)..(15)

<223> unnatural aromatic amino acid or any unnatural
hydroxy containing amino acid; Xaa at residue 15
is des-Xaa11, Gln, Asn, Leu (D or L), Ile, Val,
Ala, Gly, Trp (D or L), neo-Trp, halo-Trp (D or
L), Arg,

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<221> PEPTIDE
<222> (15)..(16)
<223> homoarginine, ornithine, Lys, N-methy-Lys,
      N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any
      unnatural basic amino acid or any unnatural
      aromatic amino acid; Xaa at residue 16 is des-Xaa,
      Ala, Gly, Phe,

<220>
<221> PEPTIDE
<222> (16)..(17)
<223> Trp (D or L), neo-Trp, halo-Trp (D or L) or any
      unnatural aromatic amino acid; Xaa at residue 17
      is des-Xaa, Glu, Gla, Asp, Phe or any unnatural
      aromatic amino acid.

<220>
<221> PEPTIDE
<222> (18)..(19)
<223> Xaa at residue 18 is des-Xaa, Ile, Val or Leu (D
      or L); Xaa at residue 19 is des-Xaa, Thr, Ser,
      Arg, homoarginine, ornithine, Lys, N-methy-Lys,
      N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any
      unnatural

<220>
<221> PEPTIDE
<222> (19)..(22)
<223> basic amino acid; Xaa at residue 20 is des-Xaa,
      Glu, Gla or Asp; Xaa at residue 21 is des-Xaa, Asn
      or Gln; Xaa at residue 22 is des-Xaa, Asp, Glu or
      Gla.

<220>
<221> PEPTIDE
<222> (23)
<223> Xaa at residue 23 is des-Xaa, Phe or any unnatural
      aromatic amino acid.

<400> 1
Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa
    1           5           10          15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    20

<210> 2
<211> 11
<212> PRT
<213> Conus aulicus

<220>
<221> PEPTIDE
<222> (4)..(8)
<223> Xaa at residue 4 is Pro or hydroxy-Pro; Xaa at
      residue 8 is Tyr, nor-Tyr, mono-halo-Tyr,
      di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
      nitro-Tyr.

<220>
<221> PEPTIDE
<222> (11)
<223> Xaa at residue 11 is Trp (D or L), neo-Trp or

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halo-Trp (D or L).

<400> 2
 Phe Cys Cys Xaa Val Ile Arg Xaa Cys Cys Xaa
 1 5 10

<210> 3
 <211> 11
 <212> PRT
 <213> Conus aulicus

<220>
 <221> PEPTIDE
 <222> (4)..(8)
 <223> Xaa at residue 4 is Pro or hydroxy-Pro; Xaa at
 residue 8 is Tyr, nor-Tyr, mono-halo-Tyr,
 di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
 nitro-Tyr.

<220>
 <221> PEPTIDE
 <222> (11)
 <223> Xaa at residue 11 is Trp (D or L), neo-Trp or
 halo-Trp (D or L).

<400> 3
 Phe Cys Cys Xaa Phe Ile Arg Xaa Cys Cys Xaa
 1 5 10

<210> 4
 <211> 10
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (6)..(7)
 <223> Xaa at residue 6 is Tyr, mono-halo-Tyr,
 di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
 nitro-Tyr; Xaa at residue 7 is Trp (D or L),
 neo-Trp or halo-Trp (D or L).

<400> 4
 Cys Cys Gln Thr Phe Xaa Xaa Cys Cys Gln
 1 5 10

<210> 5
 <211> 13
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(3)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at
 residue 3 is Trp (D or L), neo-Trp or halo-Trp (D
 or L); Xaa at residue 6 is Lys, N-methyl-Lys,
 N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<220>
 <221> PEPTIDE

<222> (7)
<223> Xaa at residue 7 is Glu or gamma-carboxy-Glu.

<400> 5
Xaa Gly Xaa Cys Cys Xaa Xaa Asn Ile Ala Cys Cys Ile
1 5 10

<210> 6
<211> 10
<212> PRT
<213> Conus querceanus

<400> 6
Gly Cys Cys Ala Arg Leu Thr Cys Cys Val
1 5 10

<210> 7
<211> 12
<212> PRT
<213> Conus purpurascens

<220>
<221> PEPTIDE
<222> (5)..(6)
<223> Xaa at residue 5 is Pro or hydroxy-Pro; Xaa at residue 6 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 7
Asn Gly Cys Cys Xaa Lys Gln Met Arg Cys Cys Thr
1 5 10

<210> 8
<211> 15
<212> PRT
<213> Conus imperialis

<220>
<221> PEPTIDE
<222> (2)..(15)
<223> Xaa at residues 2 and 15 is Trp (D or L), neo-Trp or halo-Trp (D or L); Xaa at residue 8 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa at residues 10 and 14 is Pro or hydroxy-Pro.

<400> 8
Asp Xaa Asn Ser Cys Cys Gly Xaa Asn Xaa Gly Cys Cys Xaa Xaa
1 5 10 15

<210> 9
<211> 13
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(6)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 2 is Trp (D or L), neo-Trp or halo-Trp (D

or L); Xaa at residue 6 is Lys, N-methyl-Lys,
N,N,-dimethyl-Lys or N,N,N-trimethyl-Lys.

<220>

<221> PEPTIDE

<222> (7)

<223> Xaa at residue 7 is Glu or gamma-carboxy-Glu.

<400> 9

Xaa	Gly	Xaa	Cys	Cys	Xaa	Xaa	Asn	Ile	Arg	Cys	Cys	Val
1					5				10			

<210> 10

<211> 15

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residues 1 and 4 is Glu or
gamma-carboxy-Glu; Xaa at residue 7 is Trp (D or
L), neo-Trp or halo-Trp (D or L); Xaa at residue
13 is Pro or hydroxy-Pro.

<400> 10

Xaa	Cys	Cys	Xaa	Asp	Gly	Xaa	Cys	Cys	Thr	Ala	Ala	Xaa	Leu	Thr
1				5					10				15	

<210> 11

<211> 15

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (4)..(13)

<223> ; Xaa at residue 4 is Glu or gamma-carboxy-Glu;
Xaa at residue 7 is Trp (D or L) neo-Trp or
halo-Trp (D or L); Xaa at residue 13 is Pro or
hydroxy-Pro.

<400> 11

Gly	Cys	Cys	Xaa	Asp	Gly	Xaa	Cys	Cys	Thr	Ala	Ala	Xaa	Leu	Thr
1				5					10				15	

<210> 12

<211> 20

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (14)..(17)

<223> Xaa at residue 14 and 17 is Glu or
gamma-carboxy-Glu; Xaa at residue 16 is Lys,
N-methyl-Lys, N,N-dimethyl-Lys or
N,N,N-trimethyl-Lys.

<400> 12

Asn	Gly	Cys	Cys	Arg	Ala	Gly	Asp	Cys	Cys	Ser	Arg	Phe	Xaa	Ile	Xaa
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1

5

10

15

Xaa Asn Asp Phe
20

<210> 13
<211> 10
<212> PRT
<213> Conus marmoreus

<400> 13
Asn Ala Cys Cys Ile Val Arg Gln Cys Cys
1 5 10

<210> 14
<211> 11
<212> PRT
<213> Conus marmoreus

<400> 14
Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser
1 5 10

<210> 15
<211> 11
<212> PRT
<213> Conus characteristicus

<220>
<221> PEPTIDE
<222> (3)
<223> Xaa at residue 3 is Pro or hydroxy-Pro.

<400> 15
Cys Cys Xaa Arg Arg Leu Ala Cys Cys Ile Ile
1 5 10

<210> 16
<211> 10
<212> PRT
<213> Conus characteristicus

<220>
<221> PEPTIDE
<222> (3)..(6)
<223> Xaa at residue 3 and 6 is Pro or hydroxy-Pro; Xaa
at residue 5 is Lys, N-methyl-Lys,
N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 16
Cys Cys Xaa Asn Xaa Xaa Cys Cys Phe Ile
1 5 10

<210> 17
<211> 10
<212> PRT
<213> Conus quercinus

<400> 17

Gly Cys Cys Ala Met Leu Thr Cys Cys Val
 1 5 10

<210> 18
 <211> 13
 <212> PRT
 <213> Conus gloriamaris

 <220>
 <221> PEPTIDE
 <222> (6)..(13)
 <223> Xaa at residue 6 and 11 is Glu or
 gamma-carboxy-Glu; Xaa at residues 8, 12 and 13 is
 Trp (D or L), neo-Trp or halo-Trp (D or L).

<400> 18
 Leu Cys Cys Val Thr Xaa Asp Xaa Cys Cys Xaa Xaa Xaa
 1 5 10

<210> 19
 <211> 11
 <212> PRT
 <213> Conus gloriamaris

 <220>
 <221> PEPTIDE
 <222> (5)
 <223> Xaa at residue 5 is Pro or hydroxy-Pro.

<400> 19
 Val Cys Cys Arg Xaa Val Gln Asp Cys Cys Ser
 1 5 10

<210> 20
 <211> 554
 <212> DNA
 <213> Conus textile

 <220>
 <221> CDS
 <222> (65)..(250)

 <400> 20
 ggtaactcaac gaacttcaag acacattctt ttcacacctgga cacgggaagc tgactacaag 60
 caga atg tgc tgt ctc cca gtg ttc gtc att ctt ctg ctg ctg att gca 109
 Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Ala
 1 5 10 15
 tct gca cct agc gtt gat gcc caa ccg aag acc aaa gat gat gtg ccc 157
 Ser Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro
 20 25 30
 ctg gca cct ttg cac gat aat gca aag agt gca cta caa cat ttg aac 205
 Leu Ala Pro Leu His Asp Asn Ala Lys Ser Ala Leu Gln His Leu Asn
 35 40 45
 caa cgc tgc tgc caa aca ttc tat tgg tgc tgt gtt caa ggg aaa 250
 Gln Arg Cys Cys Gln Thr Phe Tyr Trp Cys Cys Val Gln Gly Lys
 50 55 60

tgaatttgaa tgagaccctt gcgaactgtc catggatgtg agatttggaa agcagactgt 310
 tccttcgca cgtgttcgtg gaattttgaa tggtcgttaa caacacgctg ccacttgcaa 370
 gctactatct ctctgtcctt tcatactgtgg aactggatga cctaacaact gaaatatcat 430
 agaaaattttt cagtgggtat acactatgac catgttagtca gtaattacat catttggacc 490
 ttttggaaata tttttcaaaa tgttaagatt tttcccccng gaaaggnc ttgaagtaaa 550
 tatt 554

<210> 21
 <211> 62
 <212> PRT
 <213> Conus textile

<400> 21
 Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Ala Ser
 1 5 10 15
 Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30
 Ala Pro Leu His Asp Asn Ala Lys Ser Ala Leu Gln His Leu Asn Gln
 35 40 45
 Arg Cys Cys Gln Thr Phe Tyr Trp Cys Cys Val Gln Gly Lys
 50 55 60

<210> 22
 <211> 416
 <212> DNA
 <213> Conus geographus

<220>
 <221> CDS
 <222> (1)...(183)

<400> 22
 atg tgc tgt ctc cca gtc ttc gtc att ctt ctg ttg ctg att aca tct 48
 Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Thr Ser
 1 5 10 15
 gca cct agc gtt gat gct cta ccg aag acc agg gat gat gtg ccc cta 96
 Ala Pro Ser Val Asp Ala Leu Pro Lys Thr Arg Asp Asp Val Pro Leu
 20 25 30
 gca tct ttc cac ggt gga tat aat gca agg aga atc cta caa agg cgt 144
 Ala Ser Phe His Gly Gly Tyr Asn Ala Arg Arg Ile Leu Gln Arg Arg
 35 40 45
 cag ggc tgg tgc tgc aaa gaa aat att gcg tgc tgt ata tagtgtaac 193
 Gln Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Ile
 50 55 60
 gggaaatgac tttggatgag acccctgcaa actgtccctg gatgtgaaat ttggaaagta 253
 gactgttcct ttcgcgcgtg ttcgtgaaat ttcaaatttgt cgtaacaac acactgctac 313
 ttgcaaaagct actatctctc tgcctttca tctgtgaaac tgggtgatct aacagctgaa 373

atgtcgcaga aattttcaa ttggctata ctatgaccat gta 416

<210> 23
<211> 61
<212> PRT
<213> Conus geographus

<400> 23
Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Thr Ser
1 5 10 15
Ala Pro Ser Val Asp Ala Leu Pro Lys Thr Arg Asp Asp Val Pro Leu
20 25 30
Ala Ser Phe His Gly Gly Tyr Asn Ala Arg Arg Ile Leu Gln Arg Arg
35 40 45
Gln Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Ile
50 55 60

<210> 24
<211> 413
<212> DNA
<213> Conus quercinus

<220>
<221> CDS
<222> (1)..(186)

<400> 24
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Met Arg Cys Val Pro Val Phe Ile Ile Leu Leu Leu Ser Pro Ser
1 5 10 15
gca cct agc gtt gat gcc cat ccg atg acc aaa gat gat gtg ccc cag 96
Ala Pro Ser Val Asp Ala His Pro Met Thr Lys Asp Asp Val Pro Gln
20 25 30
gca tca ttc cat gat gat gca aag cga acc cta caa gta cct tgg atg 144
Ala Ser Phe His Asp Asp Ala Lys Arg Thr Leu Gln Val Pro Trp Met
35 40 45
aaa cgc ggg tgc tgc gca agg ttg act tgc tgc gtt gga cga 186
Lys Arg Gly Cys Cys Ala Arg Leu Thr Cys Cys Val Gly Arg
50 55 60

taaaggaaaa tgactttgga tgagaccct gcgaactgtc cctggatgtg aaatttggac 246
agcagactgc tccttcgca cgtgttcgtg gaattttgaa tggtcgttaa caacacgctg 306
ccacttgcaa gctattatct ctctgtccct ttatctgtgg aactggataa tctaacaact 366
gaaaatgtcat tgaaaatttt caatggatat atattatgat ccatata 413

<210> 25
<211> 62
<212> PRT
<213> Conus quercinus

<400> 25
Met Arg Cys Val Pro Val Phe Ile Ile Leu Leu Leu Ser Pro Ser

1

5

10

15

Ala Pro Ser Val Asp Ala His Pro Met Thr Lys Asp Asp Val Pro Gln
 20 25 30

Ala Ser Phe His Asp Asp Ala Lys Arg Thr Leu Gln Val Pro Trp Met
 35 40 45

Lys Arg Gly Cys Cys Ala Arg Leu Thr Cys Cys Val Gly Arg
 50 55 60

<210> 26

<211> 435

<212> DNA

<213> Conus imperialis

<220>

<221> CDS

<222> (26)..(211)

<400> 26

aattcggaa ctgactacaa gcaga atg tac tgt ctc cca gtc ttc atc att 52
 Met Tyr Cys Leu Pro Val Phe Ile Ile
 1 5

ctt ctg ctg ctg att tca tct gca cct agc act cct ccc caa cca agg 100
 Leu Leu Leu Leu Ile Ser Ser Ala Pro Ser Thr Pro Pro Gln Pro Arg
 10 15 20 25

aac aaa gat cgt gtg cac ctg ata tct tta ctc gat aat cac aag caa 148
 Asn Lys Asp Arg Val His Leu Ile Ser Leu Leu Asp Asn His Lys Gln
 30 35 40

atc cta caa aga gat tgg aac agt tgc tgt ggg aaa aat cct ggt tgc 196
 Ile Leu Gln Arg Asp Trp Asn Ser Cys Cys Gly Lys Asn Pro Gly Cys
 45 50 55

tgt cct tgg gga aaa tgactttgga tgagaccctt gcaaactgtc cctggatgtg 251
 Cys Pro Trp Gly Lys
 60

agatttggaa agcagaccgt ttgtgaaatt ttgaatggtc gttaacaaca cgctgccact 311

tgcaagctac aatctctctg tccttcatc tttggactg gatgatcaa caactgaaat 371

gtcatagaaa ttttcaatg ggtatacaat atgtggcat ttagtcagta attacatcat 431

ttgg 435

<210> 27

<211> 62

<212> PRT

<213> Conus imperialis

<400> 27

Met Tyr Cys Leu Pro Val Phe Ile Ile Leu Leu Leu Ile Ser Ser
 1 5 10 15

Ala Pro Ser Thr Pro Pro Gln Pro Arg Asn Lys Asp Arg Val His Leu
 20 25 30

Ile Ser Leu Leu Asp Asn His Lys Gln Ile Leu Gln Arg Asp Trp Asn

35

40

45

Ser Cys Cys Gly Lys Asn Pro Gly Cys Cys Pro Trp Gly Lys
 50 55 60

<210> 28
 <211> 421
 <212> DNA
 <213> Conus geographus

<220>
 <221> CDS
 <222> (1)..(183)

<400> 28
 atg tgc tgt ctc cca gtc ttc gtc att ctt ctg ttg ctg att aca tct 48
 Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Thr Ser
 1 5 10 15

gca cct agc gtt gat gct cta ccg aag acc agg gat gat gtg ccc cta 96
 Ala Pro Ser Val Asp Ala Leu Pro Lys Thr Arg Asp Asp Val Pro Leu
 20 25 30

gca tct ttc cac ggt gga tat aat gca agg aga atc cta caa agg cgt 144
 Ala Ser Phe His Gly Gly Tyr Asn Ala Arg Arg Ile Leu Gln Arg Arg
 35 40 45

cag ggc tgg tgc tgc aaa gaa aat att gcg tgc tgt gta tagtgtaac 193
 Gln Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Val
 50 55 60

gggaaatgac tttggatgag acccctgcaa actgtccctg gatgtgaaat ttggaaagta 253
 gactgttcct ttgcgcgtg ttctgtggaat ttcaaatggc cgtcaacaac acactgctac 313
 ttgc当地 actatctctc tgccttca tctgtggaac tgggtgatct aacagctgaa 373
 atgtcgcaga aattttcaa ttggtctata ctatgaccat gtatcag 421

<210> 29
 <211> 61
 <212> PRT
 <213> Conus geographus

<400> 29
 Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Thr Ser
 1 5 10 15

Ala Pro Ser Val Asp Ala Leu Pro Lys Thr Arg Asp Asp Val Pro Leu
 20 25 30

Ala Ser Phe His Gly Gly Tyr Asn Ala Arg Arg Ile Leu Gln Arg Arg
 35 40 45

Gln Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Val
 50 55 60

<210> 30
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 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (1)..(201)

<400> 30
 atg cgc tgt ttc cca gtc ttc atc att ctt ctg ctg cta att gca tct
 Met Arg Cys Phe Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
 1 5 10 15
 gca cct tgc ttt gat gcc cga acg aag acc gat gat gat gtg ccc ctg
 Ala Pro Cys Phe Asp Ala Arg Thr Lys Thr Asp Asp Asp Val Pro Leu
 20 25 30
 tca tct ctc cgc gat aat cta aag cga acg ata cga aca cgc ctg aac
 Ser Ser Leu Arg Asp Asn Leu Lys Arg Thr Ile Arg Thr Arg Leu Asn
 35 40 45
 ata cgc gag tgc tgc gag gat gga tgg tgc tgt act gct gca ccc tta
 Ile Arg Glu Cys Cys Glu Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu
 50 55 60
 aca ggt cgt tagggataaa ggaaaaatggc tttggatgag acccctgcga
 Thr Gly Arg
 65
 attgtccctg gatgtgagat ttggaaagca gactgttccct ttcgcacgtg ttcgtggat 301
 ttcgaatggc cgtaacaac acgctgccac ttgcaagcca ccatctctct gtcctttcg 361
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 tgatcgata 431

<210> 31
 <211> 67
 <212> PRT
 <213> Conus textile

<400> 31
 Met Arg Cys Phe Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
 1 5 10 15
 Ala Pro Cys Phe Asp Ala Arg Thr Lys Thr Asp Asp Asp Val Pro Leu
 20 25 30
 Ser Ser Leu Arg Asp Asn Leu Lys Arg Thr Ile Arg Thr Arg Leu Asn
 35 40 45
 Ile Arg Glu Cys Cys Glu Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu
 50 55 60
 Thr Gly Arg
 65

<210> 32
 <211> 441
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (1)..(201)

<400> 32
atg cgc tgt ttc cca gtc ttc atc att ctt ctg ttg cta att gca tct 48
Met Arg Cys Phe Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
1 5 10 15

gca cct tgc ttt gat gcc cga acg aag acc gat gat gat gtg ccc ctg 96
Ala Pro Cys Phe Asp Ala Arg Thr Lys Thr Asp Asp Asp Val Pro Leu
20 25 30

tca tct ctc cgc gat aat cta aag cga acg ata cga aca cgc ctg aac 144
Ser Ser Leu Arg Asp Asn Leu Lys Arg Thr Ile Arg Thr Arg Leu Asn
35 40 45

ata cgc ggg tgc tgc gag gat gga tgg tgc tgt act gct gca ccc tta 192
Ile Arg Gly Cys Cys Glu Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu
50 55 60

aca ggt cgt tagggataaa ggaaaatggc tttggatgag acccctgcaa 241
Thr Gly Arg
65

attgtccctg gatgtgagat ttggaaagca gactgttccct ttgcgcacgtg ttctgtggaaat 301
ttcgaatggt cgtaacaac acgctgccac ttgcaagcca ccatctctct gtcctttcgat 361
atgtggaact gtatgatcta acaactgaaa tgtcagaaag ttttcagtgg gtatacacta 421
tgatcgtata gtcagtaatt 441

<210> 33
<211> 67
<212> PRT
<213> Conus textile

<400> 33
Met Arg Cys Phe Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser 48
1 5 10 15

Ala Pro Cys Phe Asp Ala Arg Thr Lys Thr Asp Asp Asp Val Pro Leu
20 25 30

Ser Ser Leu Arg Asp Asn Leu Lys Arg Thr Ile Arg Thr Arg Leu Asn
35 40 45

Ile Arg Gly Cys Cys Glú Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu
50 55 60

Thr Gly Arg
65

<210> 34
<211> 416
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (1)..(210)

<400> 34
atg cgc tgc ctc cca gtc ttc gtc att ctt ctg ctg ctg att gca tct 48
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Ala Ser

1

5

10

15

gca cct agc gtt gat gcc cga ccg aag acc aaa gat gat atg ccc ctg 96
 Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Met Pro Leu
 20 25 30

gca tct ttc cat gat aat gca aag cga atc ctg caa ata ctt cag gac 144
 Ala Ser Phe His Asp Asn Ala Lys Arg Ile Leu Gln Ile Leu Gln Asp
 35 40 45

aga aat ggt tgc tgc aga gca gga gac tgc tgt tca cga ttt gag ata 192
 Arg Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser Arg Phe Glu Ile
 50 55 60

aag gaa aat gac ttt gga tgagaccct gcaaactgtc cttggatgtg 240
 Lys Glu Asn Asp Phe Gly
 65 70

agatttggaa agcagactgt tccttcgca cgtgttcgtg gaatttcgaa tggtcgttaa 300
 caaacacgctg ccacttgcaa gctactatct ctctgtcctt ttgtctgtgg aactgttatga 360
 tcaaacaact gaaatgtcat agaaattttt cagtggtaa acactatgac catgta 416

<210> 35

<211> 70

<212> PRT

<213> Conus marmoreus

<400> 35

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Ala Ser
 1 5 10 15

Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Met Pro Leu
 20 25 30

Ala Ser Phe His Asp Asn Ala Lys Arg Ile Leu Gln Ile Leu Gln Asp
 35 40 45

Arg Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser Arg Phe Glu Ile
 50 55 60

Lys Glu Asn Asp Phe Gly
 65 70

<210> 36

<211> 487

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (3)...(179)

<400> 36

ga atg cgc tgc ctc cca gtc ttc gtc att ctt ctg ctg ctg att gca 47
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Ala
 1 5 10 15

tct gca cct agc gtt gat gcc cga ccg aag acc aaa gat gat atg ccc 95
 Ser Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Met Pro
 20 25 30

ctg gca tct ttc cac gat aat gca aag cga atc ctg caa ata ctt cag 143
 Leu Ala Ser Phe His Asp Asn Ala Lys Arg Ile Leu Gln Ile Leu Gln
 35 40 45

gac aga aat gct tgc tgc ata gta agg cag tgc tgt tgatgatttg 189
 Asp Arg Asn Ala Cys Cys Ile Val Arg Gln Cys Cys
 50 55

agataaaagga aaatgacttt ggatgagacc cctgcaaact gtccctggat gtgagatttg 249
 gaaagcagac tgcccttgc gcacgtgtc gtggatttc gaatggcgt taacaacacg 309
 ctgccacttg caagctacta tctctctgtc cttcatctg tggaactgta tgatcaaaca 369
 actgaaatgt catagaaatt tttcagtggg taaacactat gatcatgtag tcagtaatta 429
 catcatttg aattccatca agcttatcga taccgtcgac ctcgaggggg ggcccggt 487

<210> 37

<211> 59

<212> PRT

<213> Conus marmoreus

<400> 37

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Ala Ser
 1 5 10 15

Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Met Pro Leu
 20 25 30

Ala Ser Phe His Asp Asn Ala Lys Arg Ile Leu Gln Ile Leu Gln Asp
 35 40 45

Arg Asn Ala Cys Cys Ile Val Arg Gln Cys Cys
 50 55

<210> 38

<211> 370

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (1)..(180)

<400> 38

atg cgc tgc ctc cca gtc ttt gtc att ctt ctg ctg ctg att gca tct 48
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Ala Ser
 1 5 10 15

gca cct agc gtt gat gcc cga ccg aag acc aaa gat gat atg ccc ctg 96
 Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Met Pro Leu
 20 25 30

gca tct ttc cat gat aat gca aag cga atc ctg caa ata ctt cag gac 144
 Ala Ser Phe His Asp Asn Ala Lys Arg Ile Leu Gln Ile Leu Gln Asp
 35 40 45

aga aat ggt tgc tgc aga gca gga gac tgc tgt tca tgatggaga 190
 Arg Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser
 50 55 60

taaaggaa tgactttgga tgagaccctt gcaaactgtc cttggatgtg agatttggaa 250
 agcagactgt tccttcgca cgtgttcgtg gaatttcgaa tggtcgttaa caacacgctg 310
 ccacttgcaa gctactatct ctctgtcctt tcatctgtgg aactgtatga tcaaacaact 370

<210> 39
 <211> 60
 <212> PRT
 <213> Conus marmoreus

<400> 39
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Ala Ser
 1 5 10 15
 Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Met Pro Leu
 20 25 30
 Ala Ser Phe His Asp Asn Ala Lys Arg Ile Leu Gln Ile Leu Gln Asp
 35 40 45
 Arg Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser
 50 55 60

<210> 40
 <211> 413
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (1)..(192)

<400> 40
 atg cgc tgt ctc ccg gtc ttc atc att ctt ctg ctg ctg att gca tct 48
 Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Leu Ile Ala Ser
 1 5 10 15
 gca cct ggc gtt gat gcc caa ccg aag acc aaa tat aat gcg ccc ctg 96
 Ala Pro Gly Val Asp Ala Gln Pro Lys Thr Lys Tyr Asn Ala Pro Leu
 20 25 30
 aca tct ctc cac gat aat gca aag ggt ata cta caa gaa cat tgg aac 144
 Thr Ser Leu His Asp Asn Ala Lys Gly Ile Leu Gln Glu His Trp Asn
 35 40 45
 aaa cgc tgc tgc ccc aga agg ctt gcc tgc tgt att ata gga cgg aaa 192
 Lys Arg Cys Cys Pro Arg Arg Leu Ala Cys Cys Ile Ile Gly Arg Lys
 50 55 60
 tgaatgattt tgggtgagat ccctgcaaac tgtccctgga tttgaatttt ggaaaggaga 252
 ctgttccttt cgcacgtgtt cgtggaaattt cgaatggtcg ttaacaacac gctgccactt 312
 gcaagctact atctctctgt ccttttctc tgtgaaaactg gatggctaa caactgaaat 372
 gtcatagaaa atttcaatg ggtatactct atgaccatct a 413

<210> 41
 <211> 64
 <212> PRT

<213> Conus characteristicus

<400> 41
 Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
 1 5 10 15
 Ala Pro Gly Val Asp Ala Gln Pro Lys Thr Lys Tyr Asn Ala Pro Leu
 20 25 30
 Thr Ser Leu His Asp Asn Ala Lys Gly Ile Leu Gln Glu His Trp Asn
 35 40 45
 Lys Arg Cys Cys Pro Arg Arg Leu Ala Cys Cys Ile Ile Gly Arg Lys
 50 55 60

<210> 42

<211> 410

<212> DNA

<213> Conus characteristicus

<220>
<221> CDS
<222> (1)..(189)

<400> 42
 atg cgc tgt ctc cca gtc ttc atc att ctt ctg ctg ctg att gca tct 48
 Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
 1 5 10 15
 gca cct ggc gtt gat gcc caa ccg aag acc aaa tat gat gcg ccc ctg 96
 Ala Pro Gly Val Asp Ala Gln Pro Lys Thr Lys Tyr Asp Ala Pro Leu
 20 25 30
 aca tct ctc cac gat aat gca aag ggt ata cta caa gaa cat tgg aac 144
 Thr Ser Leu His Asp Asn Ala Lys Gly Ile Leu Gln Glu His Trp Asn
 35 40 45
 aaa cgc tgc tgc ccc aac aag cct tgc tgt ttt ata gga agg aaa 189
 Lys Arg Cys Cys Pro Asn Lys Pro Cys Cys Phe Ile Gly Arg Lys
 50 55 60
 tgaatgattt tgggtgagac ccctgcaaac tgtccctgga tttgaatttt ggaaaggcaga 249
 ctgttccttt cgcacgtgtt cgtgaaattt cgaatggtcg ttaacaacac gctgccactt 309
 gcaagctact atctctctgt ccttttctc tgtgaaaactg gatggtctaa caactgagat 369
 gtcatagaaa atttcaatc ggtgtactct atgaccatct a 410

<210> 43

<211> 63

<212> PRT

<213> Conus characteristicus

<400> 43
 Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
 1 5 10 15
 Ala Pro Gly Val Asp Ala Gln Pro Lys Thr Lys Tyr Asp Ala Pro Leu
 20 25 30
 Thr Ser Leu His Asp Asn Ala Lys Gly Ile Leu Gln Glu His Trp Asn

35

40

45

Lys	Arg	Cys	Cys	Pro	Asn	Lys	Pro	Cys	Cys	Phe	Ile	Gly	Arg	Lys
50					55					60				

<210> 44
<211> 413
<212> DNA
<213> Conus quercinus

<220>
<221> CDS
<222> (1)..(186)

<400> 44
atg cgc tgt gtc cca gtc ttc atc att ctt ctg ctg agt cca tct 48
Met Arg Cys Val Pro Val Phe Ile Ile Leu Leu Leu Ser Pro Ser
1 5 10 15

gca cct agc gtt gat gcc cat ccg atg acc aaa gat gat gta ccc cag 96
Ala Pro Ser Val Asp Ala His Pro Met Thr Lys Asp Asp Val Pro Gln
20 25 30

gca tct ctc cat gat gat gca aag cga acc cta caa gta cct tgg atg 144
Ala Ser Leu His Asp Asp Ala Lys Arg Thr Leu Gln Val Pro Trp Met
35 40 45

aaa cgc ggg tgc tgc gca atg ttg act tgc tgc gtt gga cga 186
Lys Arg Gly Cys Cys Ala Met Leu Thr Cys Cys Val Gly Arg
50 55 60

taaaggaaaa tgactttgga tgagaccct acgaactgtc cctggatgtg aaatttggac 246
agcagactgc tccttcgca cgtgttcgtg gaatttcgaa tggtcgttaa caacacgctg 306
ccacttgcaa gctattatct ctctgtccct ttatctgtgg aactggataa tctaacaact 366
gaaacgtcat tgaaaatttt caatggatat atattatgat ccatata 413

<210> 45
<211> 62
<212> PRT
<213> Conus quercinus

<400> 45
Met Arg Cys Val Pro Val Phe Ile Ile Leu Leu Leu Ser Pro Ser
1 5 10 15

Ala Pro Ser Val Asp Ala His Pro Met Thr Lys Asp Asp Val Pro Gln
20 25 30

Ala Ser Leu His Asp Asp Ala Lys Arg Thr Leu Gln Val Pro Trp Met
35 40 45

Lys Arg Gly Cys Cys Ala Met Leu Thr Cys Cys Val Gly Arg
50 55 60

<210> 46
<211> 735
<212> DNA
<213> Conus gloriamaris

<220>
<221> CDS
<222> (70)..(258)

<400> 46
gggcaggtac tcaacgaact tcaggacaca ttctttcac ctggacacgg gaaactgact 60
ataaggaga atg cgc tac cta cca gtc ttc gtc att ctt ctg ctg ctg att 111
Met Arg Tyr Leu Pro Val Phe Val Ile Leu Leu Leu Ile
1 5 10
gca tct ata cct agc gat act gtc caa ctg aag acc aaa gat gat atg 159
Ala Ser Ile Pro Ser Asp Thr Val Gln Leu Lys Thr Lys Asp Asp Met
15 20 25 30
ccc ctg gca tct ttc cac ggt aat gga aga cga atc ctg cga atg ctt 207
Pro Leu Ala Ser Phe His Gly Asn Gly Arg Arg Ile Leu Arg Met Leu
35 40 45
tca aac aaa cgc tta tgc tgt gtc acc gag gat tgg tgc tgt gaa tgg 255
Ser Asn Lys Arg Leu Cys Cys Val Thr Glu Asp Trp Cys Cys Glu Trp
50 55 60
tgg taaaggaaaa tgactttgga tgagaccct gcaaactgtt tctggatgtg 308
Trp
agatttggaa agcagactgt tcttcgcac gtattcgtga aatttcgaat ggtcgttaac 368
aacacgctgc cacttgcaag ctgctatctc tctgtcttt catctgtgga actgtatgtat 428
ctaacaactg aaatgtcata gacattttc attgggtata cactatgacc atgttagccag 488
taattacatc atttggacct tttggatatt tttcagtatg taagtgtgtt cccttaaaaa 548
gtcctttgta attatgtatt ttaanaattt angtttgca cataaattgt aaaacgctgt 608
cctttctgtt gntcctacat cantgggtgg gaaaagnaaa atgtttgcc ntggtaaat 668
ttaaataatn accctgccgt tttaatgcng ttattantgg tattttnaac nttgnacgg 728
taaactt 735

<210> 47
<211> 63
<212> PRT
<213> Conus gloriamaris

<400> 47
Met Arg Tyr Leu Pro Val Phe Val Ile Leu Leu Leu Ile Ala Ser 15
1 5 10 15
Ile Pro Ser Asp Thr Val Gln Leu Lys Thr Lys Asp Asp Met Pro Leu
20 25 30
Ala Ser Phe His Gly Asn Gly Arg Arg Ile Leu Arg Met Leu Ser Asn
35 40 45
Lys Arg Leu Cys Cys Val Thr Glu Asp Trp Cys Cys Glu Trp Trp
50 55 60

<210> 48
<211> 374

<212> DNA

<213> Conus gloriamaris

<220>

<221> CDS

<222> (3)...(188)

<400> 48

ga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg ctg ctg att gca	47
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala	
1 5 10 15	

tct gca cct agc gtt gat gcc caa ccg aag acc aaa gat gat gtg ccc	95
Ser Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro	
20 25 30	

ctg gca cct ttg cac gat aat ata agg agt act cta caa aca ctt cg	143
Leu Ala Pro Leu His Asp Asn Ile Arg Ser Thr Leu Gln Thr Leu Arg	
35 40 45	

aag aaa gtc tgc tgc cgc cca gtg cag gat tgc tgt tca ggg aaa	188
Lys Lys Val Cys Cys Arg Pro Val Gln Asp Cys Ser Gly Lys	
50 55 60	

tgaaggaaa tgaatttggaa tgagaccct gcgaactgtc cctggatgtg agatttgaa	248
agcagactgt tccttcgca cgtgttcgtg gaatttcgaa tggtcgttaa caacacgctg	308
ccacttgcaa gctactatct ctctgtcctt tcatctgcgg aactggatga cctaaagctt	368
gtgatc	374

<210> 49

<211> 62

<212> PRT

<213> Conus gloriamaris

<400> 49

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala Ser	
1 5 10 15	

Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro Leu	
20 25 30	

Ala Pro Leu His Asp Asn Ile Arg Ser Thr Leu Gln Thr Leu Arg Lys	
35 40 45	

Lys Val Cys Cys Arg Pro Val Gln Asp Cys Cys Ser Gly Lys	
50 55 60	